

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/573,130
Source: TEUP
Date Processed by STIC: 4-4-06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>10/573/130</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWP

RAW SEQUENCE LISTING

DATE: 04/04/2006

PATENT APPLICATION: US/10/573,130

TIME: 10:13:06

Input Set : A:\Final Sequence list-13111-00035-US.txt

Output Set: N:\CRF4\04042006\J573130.raw

3 <110> APPLICANT: Sturmer, Rainer
 4 Kessler, Maria
 5 Hauer, Bernhard
 6 Friedrich, Thomas
 7 Breuer, Michael
 9 <120> TITLE OF INVENTION: Methods for the production of
 10 3-methylamino-1-(thiene-2-yl)-propane-1-ol
 12 <130> FILE REFERENCE: 13111-00035-US
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/573,130
 C--> 14 <141> CURRENT FILING DATE: 2005-03-23
 14 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/010939
 15 <151> PRIOR FILING DATE: 2004-09-30
 17 <150> PRIOR APPLICATION NUMBER: DE 103 45 772.0
 18 <151> PRIOR FILING DATE: 2003-10-01
 20 <160> NUMBER OF SEQ ID NOS: 44
 22 <170> SOFTWARE: PatentIn version 3.3
 26 <210> SEQ ID NO: 1
 28 <211> LENGTH: 47
 30 <212> TYPE: PRT
 32 <213> ORGANISM: Lactobacillus brevis
 36 <400> SEQUENCE: 1
 38 Met Ser Asn Arg Leu Asp Gly Lys Val Ala Ile Val Thr Gly Gly Thr
 39 1 5 10 15
 42 Leu Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala
 43 20 25 30
 46 Lys Val Met Ile Thr Gly Arg His Ser Asp Val Gly Glu Lys Ala
 47 35 40 45
 50 <210> SEQ ID NO: 2
 52 <211> LENGTH: 18
 54 <212> TYPE: PRT
 56 <213> ORGANISM: Candida magnoliae
 60 <400> SEQUENCE: 2
 62 Ser Asn Ala Leu Val Thr Gly Gly Ser Arg Val Ile Gly Ala Gly Gly
 63 1 5 10 15
 66 Phe Ile
 70 <210> SEQ ID NO: 3
 72 <211> LENGTH: 756
 74 <212> TYPE: DNA
 76 <213> ORGANISM: Lactobacillus brevis
 80 <220> FEATURE:
 82 <221> NAME/KEY: CDS
 84 <222> LOCATION: (1)..(756)
 88 <400> SEQUENCE: 3

Data Not Comply
 Corrected Diskette Needed

(pg.6)

(pg.7)

RAW SEQUENCE LISTING

DATE: 04/04/2006

PATENT APPLICATION: US/10/573,130

TIME: 10:13:06

Input Set : A:\Final Sequence list-13111-00035-US.txt

Output Set: N:\CRF4\04042006\J573130.raw

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89 atg tct aac cgt ttg gat gga aaa gta gca atc gtt aca ggt ggt acg      48
90 Met Ser Asn Arg Leu Asp Gly Lys Val Ala Ile Val Thr Gly Gly Thr
91 1          5          10          15
93 ttg ggt atc ggt tta gct atc gcc acg aag ttc gtt gaa gaa ggg gct      96
94 Leu Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala
95          20          25          30
97 aag gtc atg att acc ggc cgg cac agc gat gtt ggt gaa aaa gca gct      144
98 Lys Val Met Ile Thr Gly Arg His Ser Asp Val Gly Glu Lys Ala Ala
99          35          40          45
101 aag agt gtc ggc act cct gat cag att caa ttt ttc caa cat gat tct      192
102 Lys Ser Val Gly Thr Pro Asp Gln Ile Gln Phe Phe Gln His Asp Ser
103          50          55          60
105 tcc gat gaa gac ggc tgg acg aaa tta ttc gat gca acg gaa aaa gcc      240
106 Ser Asp Glu Asp Gly Trp Thr Lys Leu Phe Asp Ala Thr Glu Lys Ala
107 65          70          75          80
109 ttt ggc cca gtt tct aca tta gtt aat aac gct ggg atc gcg gtt aac      288
110 Phe Gly Pro Val Ser Thr Leu Val Asn Asn Ala Gly Ile Ala Val Asn
111          85          90          95
113 aag agt gtc gaa gaa acc acg act gct gaa tgg cgt aaa cta tta gcc      336
114 Lys Ser Val Glu Glu Thr Thr Thr Ala Glu Trp Arg Lys Leu Leu Ala
115          100          105          110
117 gtc aac ctt gat ggt gtc ttc ttc ggt acc cga tta ggg att caa cgg      384
118 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
119          115          120          125
121 atg aag aac aaa ggc tta ggg gct tcc atc atc aac atg tct tcg atc      432
122 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
123          130          135          140
125 gaa ggc ttt gtg ggt gat cct agc tta ggg gct tac aac gca tct aaa      480
126 Glu Gly Phe Val Gly Asp Pro Ser Leu Gly Ala Tyr Asn Ala Ser Lys
127 145          150          155          160
129 ggg gcc gta cgg att atg tcc aag tca gct gcc tta gat tgt gcc cta      528
130 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
131          165          170          175
133 aag gac tac gat gtt cgg gta aac act gtt cac cct ggc tac atc aag      576
134 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Tyr Ile Lys
135          180          185          190
137 aca cca ttg gtt gat gac cta cca ggg gcc gaa gaa gcg atg tca caa      624
138 Thr Pro Leu Val Asp Asp Leu Pro Gly Ala Glu Glu Ala Met Ser Gln
139          195          200          205
141 cgg acc aag acg cca atg ggc cat atc ggt gaa cct aac gat att gcc      672
142 Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
143          210          215          220
145 tac atc tgt gtt tac ttg gct tct aac gaa tct aaa ttt gca acg ggt      720
146 Tyr Ile Cys Val Tyr Leu Ala Ser Asn Glu Ser Lys Phe Ala Thr Gly
147 225          230          235          240
149 tct gaa ttt gta gtt gac ggt ggc tac act gct caa      756
150 Ser Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
151          245          250
154 <210> SEQ ID NO: 4

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RAW SEQUENCE LISTING

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Input Set : A:\Final Sequence list-13111-00035-US.txt

Output Set: N:\CRF4\04042006\J573130.raw

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156 <211> LENGTH: 252
158 <212> TYPE: PRT
160 <213> ORGANISM: Lactobacillus brevis
164 <400> SEQUENCE: 4
166 Met Ser Asn Arg Leu Asp Gly Lys Val Ala Ile Val Thr Gly Gly Thr
167 1 5 10 15
170 Leu Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala
171 20 25 30
174 Lys Val Met Ile Thr Gly Arg His Ser Asp Val Gly Glu Lys Ala Ala
175 35 40 45
178 Lys Ser Val Gly Thr Pro Asp Gln Ile Gln Phe Phe Gln His Asp Ser
179 50 55 60
182 Ser Asp Glu Asp Gly Trp Thr Lys Leu Phe Asp Ala Thr Glu Lys Ala
183 65 70 75 80
186 Phe Gly Pro Val Ser Thr Leu Val Asn Asn Ala Gly Ile Ala Val Asn
187 85 90 95
190 Lys Ser Val Glu Glu Thr Thr Thr Ala Glu Trp Arg Lys Leu Leu Ala
191 100 105 110
194 Met Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Thr Gln Arg
195 115 120 125
198 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
199 130 135 140
202 Glu Gly Phe Val Gly Asp Pro Ser Leu Gly Ala Tyr Asn Ala Ser Lys
203 145 150 155 160
206 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
207 165 170 175
210 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Tyr Ile Lys
211 180 185 190
214 Thr Pro Leu Val Asp Asp Leu Pro Gly Ala Glu Glu Ala Met Ser Gln
215 195 200 205
218 Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
219 210 215 220
222 Tyr Ile Cys Val Tyr Leu Ala Ser Asn Glu Ser Lys Phe Ala Thr Gly
223 225 230 235 240
226 Ser Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
227 245 250

```

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230 <210> SEQ ID NO: 5
232 <211> LENGTH: 472
234 <212> TYPE: DNA
236 <213> ORGANISM: Candida magnoliae
240 <220> FEATURE:
242 <221> NAME/KEY: CDS
244 <222> LOCATION: (1)..(471)
248 <400> SEQUENCE: 5
249 aac gcg ctg gtg acg ggc ggc agc cgc ggc att ggc gaa gcc act gcc 48
250 Asn Ala Leu Val Thr Gly Gly Ser Arg Gly Ile Gly Glu Ala Thr Ala
251 1 5 10 15
253 att aag ctc gcc gag gag ggc tac agc gtc acg att gcg tct cgc ggc 96
254 Ile Lys Leu Ala Glu Glu Gly Tyr Ser Val Thr Ile Ala Ser Arg Gly

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Input Set : A:\Final Sequence list-13111-00035-US.txt

Output Set: N:\CRF4\04042006\J573130.raw

```

255          20          25          30
257 ctt aag cag ctc gag gct gtg aag gcc aaa cta ccc att gtg aag cag      144
258 Leu Lys Gln Leu Glu Ala Val Lys Ala Lys Leu Pro Ile Val Lys Gln
259          35          40          45
261 gga cag gtt cac cac gtg tgg cag ctt gat ctc agt gat gtc gac gct      192
262 Gly Gln Val His His Val Trp Gln Leu Asp Leu Ser Asp Val Asp Ala
263          50          55          60
265 gcg gcc gcc ttc aaa ggg tcg ccg cta cct gcc agc cgc tac gac gtg      240
266 Ala Ala Ala Phe Lys Gly Ser Pro Leu Pro Ala Ser Arg Tyr Asp Val
267 65          70          75          80
269 ctc gtc agc aat gct ggc gtg gcc cag ttt agc ccg ttc atc gag cat      288
270 Leu Val Ser Asn Ala Gly Val Ala Gln Phe Ser Pro Phe Ile Glu His
271          85          90          95
273 gcg aag cag gac tgg tcg cag atg ctt gcc atc aat ctg gcg gca ccc      336
274 Ala Lys Gln Asp Trp Ser Gln Met Leu Ala Ile Asn Leu Ala Ala Pro
275          100          105          110
277 att gcg ctg gcc cag aca ttt gct aag gcc att ggc gac aag ccg cgc      384
278 Ile Ala Leu Ala Gln Thr Phe Ala Lys Ala Ile Gly Asp Lys Pro Arg
279          115          120          125
281 aac aca ccg gcc cac att gtg ttt gtc tcg tcg aac gtc tcg ttg cga      432
282 Asn Thr Pro Ala His Ile Val Phe Val Ser Ser Asn Val Ser Leu Arg
283          130          135          140
285 ggc ttc ccg aac atc ggc gtc aac tcc atc acc ccc ggc a      472
286 Gly Phe Pro Asn Ile Gly Val Asn Ser Ile Thr Pro Gly
287 145          150          155
290 <210> SEQ ID NO: 6
292 <211> LENGTH: 157
294 <212> TYPE: PRT
296 <213> ORGANISM: Candida magnoliae
300 <400> SEQUENCE: 6
302 Asn Ala Leu Val Thr Gly Gly Ser Arg Gly Ile Gly Glu Ala Thr Ala
303 1          5          10          15
306 Ile Lys Leu Ala Glu Glu Gly Tyr Ser Val Thr Ile Ala Ser Arg Gly
307          20          25          30
310 Leu Lys Gln Leu Glu Ala Val Lys Ala Lys Leu Pro Ile Val Lys Gln
311          35          40          45
314 Gly Gln Val His His Val Trp Gln Leu Asp Leu Ser Asp Val Asp Ala
315          50          55          60
318 Ala Ala Ala Phe Lys Gly Ser Pro Leu Pro Ala Ser Arg Tyr Asp Val
319 65          70          75          80
322 Leu Val Ser Asn Ala Gly Val Ala Gln Phe Ser Pro Phe Ile Glu His
323          85          90          95
326 Ala Lys Gln Asp Trp Ser Gln Met Leu Ala Ile Asn Leu Ala Ala Pro
327          100          105          110
330 Ile Ala Leu Ala Gln Thr Phe Ala Lys Ala Ile Gly Asp Lys Pro Arg
331          115          120          125
334 Asn Thr Pro Ala His Ile Val Phe Val Ser Ser Asn Val Ser Leu Arg
335          130          135          140
338 Gly Phe Pro Asn Ile Gly Val Asn Ser Ile Thr Pro Gly

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RAW SEQUENCE LISTING

DATE: 04/04/2006

PATENT APPLICATION: US/10/573,130

TIME: 10:13:06

Input Set : A:\Final Sequence list-13111-00035-US.txt

Output Set: N:\CRF4\04042006\J573130.raw

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339 145          150          155
343 <210> SEQ ID NO: 7
344 <211> LENGTH: 27
345 <212> TYPE: DNA
346 <213> ORGANISM: Artificial sequence
348 <220> FEATURE:
349 <223> OTHER INFORMATION: Primer: Mke 338
351 <400> SEQUENCE: 7
352 gggaattcca tatgtctaac cgtttg      27
355 <210> SEQ ID NO: 8
356 <211> LENGTH: 28
357 <212> TYPE: DNA
358 <213> ORGANISM: Artificial sequence
360 <220> FEATURE:
361 <223> OTHER INFORMATION: Primer: Mke 339
363 <400> SEQUENCE: 8
364 cgtagggaag cttattgagc agtgtagc      28
367 <210> SEQ ID NO: 9
368 <211> LENGTH: 28
369 <212> TYPE: DNA
370 <213> ORGANISM: Artificial sequence
372 <220> FEATURE:
373 <223> OTHER INFORMATION: Primer: Mke 366
375 <400> SEQUENCE: 9
376 acgacgacga gcaacgcbct bgtbacgg      28
379 <210> SEQ ID NO: 10
380 <211> LENGTH: 28
381 <212> TYPE: DNA
382 <213> ORGANISM: Artificial sequence
384 <220> FEATURE:
385 <223> OTHER INFORMATION: Primer: Mke 367
387 <400> SEQUENCE: 10
388 acgacgacgt cgaacgcbct bgtbacgg      28
391 <210> SEQ ID NO: 11
392 <211> LENGTH: 27
393 <212> TYPE: DNA
394 <213> ORGANISM: Artificial sequence
396 <220> FEATURE:
397 <223> OTHER INFORMATION: Primer: Mke 374
399 <400> SEQUENCE: 11
400 gccggggttg atsswggttsa cgccgat      27
403 <210> SEQ ID NO: 12
404 <211> LENGTH: 10
405 <212> TYPE: PRT
406 <213> ORGANISM: Lactobacillus brevis
409 <220> FEATURE:
410 <221> NAME/KEY: MISC_FEATURE
411 <222> LOCATION: (1)..(10)
412 <223> OTHER INFORMATION: Fragment: C terminus

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Page 6

<210> 15
<211> 60
<212> PRT
<213> Lactobacillus brevis

<220>
<221> VARIANT
<222> (47)..(47)
<223> Amino acid is Ala or Lys

<220>
<221> UNSURE
<222> (48)..(48)
<223> Amino acid is Lys or Ala

<220>
<221> VARIANT
<222> (53)..(53)
<223> Amino acid is Pro or Thr

<220>
<221> VARIANT
<222> (59)..(59)
<223> Amino acid is Phe, Val, Gly, or Asn

<220>
<221> misc_feature
<222> (60)..(60)
<223> Xaa is unreadable

INVALID
Response
do you mean
UNKNOWN?

See
item
13

on error
summary
sheet.

<400> 15
Ser Asn Arg Leu Asp Gly Lys Val Ala Ile Val Thr Gly Gly Thr Leu
1 5 10 15

Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala Lys
20 25 30

Val Met Ile Thr Gly Arg His Ser Asp Val Gly Glu Lys Ala Ala Lys
35 40 45

Ser Val Gly Thr Pro Asp Gln Ile Gln Phe Phe Xaa
50 55 60

pls explain "Xaa"
location.

FYI:

"Xaa" can only
represent a
single amino
acid.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/573,130

DATE: 04/04/2006
TIME: 10:13:07

Input Set : A:\Final Sequence list-13111-00035-US.txt
Output Set: N:\CRF4\04042006\J573130.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; Xaa Pos. 60
Seq#:16; Xaa Pos. 19,20
Seq#:17; Xaa Pos. 12,13,14,15
Seq#:18; Xaa Pos. 8
Seq#:19; Xaa Pos. 9,11,12,13,14,15
Seq#:22; Xaa Pos. 6,10,11,12,13,14,15
Seq#:23; Xaa Pos. 6,12,15,16,17,18
Seq#:24; Xaa Pos. 6,10,11,12,13,14,15,16,17
Seq#:25; Xaa Pos. 16,17,18,19,20
Seq#:26; Xaa Pos. 1,3
Seq#:27; Xaa Pos. 9,13
Seq#:28; Xaa Pos. 7,17,18,19,20
Seq#:30; Xaa Pos. 1,10,11,12,13,14,15,16,17,18,19,20
Seq#:32; Xaa Pos. 30
Seq#:33; Xaa Pos. 5,6,7,8,9,10
Seq#:34; Xaa Pos. 3,13,14,15,16,17,18,19,20
Seq#:35; Xaa Pos. 11,12,13,14
Seq#:36; Xaa Pos. 1
Seq#:40; Xaa Pos. 1
Seq#:41; Xaa Pos. 2,39,40
Seq#:42; Xaa Pos. 37,38,39
Seq#:43; Xaa Pos. 12,13,14,15
Seq#:44; Xaa Pos. 13,14,15

VERIFICATION SUMMARY

DATE: 04/04/2006

PATENT APPLICATION: US/10/573,130

TIME: 10:13:07

Input Set : A:\Final Sequence list-13111-00035-US.txt

Output Set: N:\CRF4\04042006\J573130.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:48
L:602 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:16
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:711 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:903 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
L:907 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:16
L:929 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:933 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:16
L:950 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:954 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:16
L:976 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:1063 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
L:1160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
L:1164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:16
L:1326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:1330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:16
L:1560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:16
L:1577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:1638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:1642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:16
L:1659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
L:1691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
L:1821 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:1851 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0
L:1859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:32
L:1993 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:32
L:2010 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:2072 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0